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RAW SEQUENCE LISTING

DATE: 09/30/2002

PATENT APPLICATION: US/10/055,797

TIME: 08:10:34

Input Set : N:\Crf3\Datahold\EFS\10055797\GNCA-P03-007SequenceListing.txt

Output Set: N:\CRF4\09302002\J055797.raw

3 <110> APPLICANT: Hammond et al.
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR RNA INTERFERENCE
 7 <130> FILE REFERENCE: GNCA-P03-007
 9 <140> CURRENT APPLICATION NUMBER: 10/055,797
 10 <141> CURRENT FILING DATE: 2002-01-22
 12 <150> PRIOR APPLICATION NUMBER: 60/189,739
 W--> 13 <151> PRIOR FILING DATE: PCT/US01/08435
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 5775
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(5775)
 27 <223> OTHER INFORMATION:
 29 <400> SEQUENCE: 1

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32	1 5 10 15	
33	atg acc cct gct tcc tca cca atg ggt cct ttc ttt gga ctg cca tgg	96
34	Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp	
35	20 25 30	
36	caa caa gaa gca att cat gat aac att tat acg cca aga aaa tat cag	144
37	Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln	
38	35 40 45	
39	gtt gaa ctg ctt gaa gca gct ctg gat cat aat acc atc gtc tgt tta	192
40	Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu	
41	50 55 60	
42	aac act ggc tca ggg aag aca ttt att gct agt act act cta cta aag	240
43	Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys	
44	65 70 75 80	
45	agc tgt ctc tat cta gat cta ggg gag act tca gct aga aat gga aaa	288
46	Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys	
47	85 90 95	
48	agg acg gtg ttc ttg gtc aac tct gca aac cag gtt gct caa caa gtg	336
49	Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val	
50	100 105 110	
51	tca gct gtc aga act cat tca gat ctc aag gtt ggg gaa tac tca aac	384
52	Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn	
53	115 120 125	
54	cta gaa gta aat gca tct tgg aca aaa gag aga tgg aac caa gag ttt	432

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55	Leu	Glu	Val	Asn	Ala	Ser	Trp	Thr	Lys	Glu	Arg	Trp	Asn	Gln	Glu	Phe	
56		130					135					140					
57	act	aag	cac	cag	ggt	ctc	att	atg	act	tgc	tat	gtc	gcc	ttg	aat	gtt	480
58	Thr	Lys	His	Gln	Val	Leu	Ile	Met	Thr	Cys	Tyr	Val	Ala	Leu	Asn	Val	
59	145					150					155					160	
60	ttg	aaa	aat	ggt	tac	tta	tca	ctg	tca	gac	att	aac	ctt	ttg	gtg	ttt	528
61	Leu	Lys	Asn	Gly	Tyr	Leu	Ser	Leu	Ser	Asp	Ile	Asn	Leu	Leu	Val	Phe	
62					165					170						175	
63	gat	gag	tgt	cat	ctt	gca	atc	cta	gac	cac	ccc	tat	cga	gaa	ttt	atg	576
64	Asp	Glu	Cys	His	Leu	Ala	Ile	Leu	Asp	His	Pro	Tyr	Arg	Glu	Phe	Met	
65					180					185					190		
66	aag	ctc	tgt	gaa	att	tgt	cca	tca	tgt	cct	cgc	att	ttg	gga	cta	act	624
67	Lys	Leu	Cys	Glu	Ile	Cys	Pro	Ser	Cys	Pro	Arg	Ile	Leu	Gly	Leu	Thr	
68					195					200					205		
69	gct	tcc	att	tta	aat	ggg	aaa	tgg	gat	cca	gag	gat	ttg	gaa	gaa	aag	672
70	Ala	Ser	Ile	Leu	Asn	Gly	Lys	Trp	Asp	Pro	Glu	Asp	Leu	Glu	Glu	Lys	
71		210					215					220					
72	ttt	cag	aaa	cta	gag	aaa	att	ctt	aag	agt	aat	gct	gaa	act	gca	act	720
73	Phe	Gln	Lys	Leu	Glu	Lys	Ile	Leu	Lys	Ser	Asn	Ala	Glu	Thr	Ala	Thr	
74	225					230					235					240	
75	gac	ctg	gtg	gtc	tta	gac	agg	tat	act	tct	cag	cca	tgt	gag	att	gtg	768
76	Asp	Leu	Val	Val	Leu	Asp	Arg	Tyr	Thr	Ser	Gln	Pro	Cys	Glu	Ile	Val	
77					245					250						255	
78	gtg	gat	tgt	gga	cca	ttt	act	gac	aga	agt	ggg	ctt	tat	gaa	aga	ctg	816
79	Val	Asp	Cys	Gly	Pro	Phe	Thr	Asp	Arg	Ser	Gly	Leu	Tyr	Glu	Arg	Leu	
80					260					265					270		
81	ctg	atg	gaa	tta	gaa	gaa	gca	ctt	aat	ttt	atc	aat	gat	tgt	aat	ata	864
82	Leu	Met	Glu	Leu	Glu	Glu	Ala	Leu	Asn	Phe	Ile	Asn	Asp	Cys	Asn	Ile	
83					275					280					285		
84	tct	gta	cat	tca	aaa	gaa	aga	gat	tct	act	tta	att	tcg	aaa	cag	ata	912
85	Ser	Val	His	Ser	Lys	Glu	Arg	Asp	Ser	Thr	Leu	Ile	Ser	Lys	Gln	Ile	
86		290					295					300					
87	cta	tca	gac	tgt	cgt	gcc	gta	ttg	gta	ggt	ctg	gga	ccc	tgg	tgt	gca	960
88	Leu	Ser	Asp	Cys	Arg	Ala	Val	Leu	Val	Val	Leu	Gly	Pro	Trp	Cys	Ala	
89	305					310					315					320	
90	gat	aaa	gta	gct	gga	atg	atg	gta	aga	gaa	cta	cag	aaa	tac	atc	aaa	1008
91	Asp	Lys	Val	Ala	Gly	Met	Met	Val	Arg	Glu	Leu	Gln	Lys	Tyr	Ile	Lys	
92					325					330					335		
93	cat	gag	caa	gag	gag	ctg	cac	agg	aaa	ttt	tta	ttg	ttt	aca	gac	act	1056
94	His	Glu	Gln	Glu	Glu	Leu	His	Arg	Lys	Phe	Leu	Leu	Phe	Thr	Asp	Thr	
95					340					345					350		
96	ttc	cta	agg	aaa	ata	cat	gca	cta	tgt	gaa	gag	cac	ttc	tca	cct	gcc	1104
97	Phe	Leu	Arg	Lys	Ile	His	Ala	Leu	Cys	Glu	Glu	His	Phe	Ser	Pro	Ala	
98					355					360					365		
99	tca	ctt	gac	ctg	aaa	ttt	gta	act	cct	aaa	gta	atc	aaa	ctg	ctc	gaa	1152
100	Ser	Leu	Asp	Leu	Lys	Phe	Val	Thr	Pro	Lys	Val	Ile	Lys	Leu	Leu	Glu	
101		370					375					380					
102	atc	tta	cgc	aaa	tat	aaa	cca	tat	gag	cga	cac	agt	ttt	gaa	agc	gtt	1200
103	Ile	Leu	Arg	Lys	Tyr	Lys	Pro	Tyr	Glu	Arg	His	Ser	Phe	Glu	Ser	Val	

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105	gag tgg tat	aat aat aga aat	cag gat aat tat	gtg tca tgg agt gat		1248		
106	Glu Trp Tyr	Asn Asn Arg Asn	Gln Asp Asn Tyr	Val Ser Trp Ser Asp				
107		405		410		415		
108	tct gag gat	gat gat gag gat	gaa gaa att gaa	gaa aaa gag aag cca		1296		
109	Ser Glu Asp	Asp Asp Glu Asp	Glu Glu Ile Glu	Glu Lys Glu Lys Pro				
110		420		425		430		
111	gag aca aat	ttt cct tct cct	ttt acc aac att	ttg tgc gga att att		1344		
112	Glu Thr Asn	Phe Pro Ser Pro	Phe Thr Asn Ile	Leu Cys Gly Ile Ile				
113		435		440		445		
114	ttt gtg gaa	aga aga tac aca	gca gtt gtc tta	aac aga ttg ata aag		1392		
115	Phe Val Glu	Arg Arg Tyr Thr	Ala Val Val Leu	Asn Arg Leu Ile Lys				
116		450		455		460		
117	gaa gct ggc	aaa caa gat cca	gag ctg gct tat	atc agt agc aat ttc		1440		
118	Glu Ala Gly	Lys Gln Asp Pro	Glu Leu Ala Tyr	Ile Ser Ser Asn Phe				
119	465		470		475		480	
120	ata act gga	cat ggc att ggg	aag aat cag cct	cgc aac aac acg atg		1488		
121	Ile Thr Gly	His Gly Ile Gly	Lys Asn Gln Pro	Arg Asn Asn Thr Met				
122		485		490		495		
123	gaa gca gaa	ttc aga aaa cag	gaa gag gta ctt	agg aaa ttt cga gca		1536		
124	Glu Ala Glu	Phe Arg Lys Gln	Glu Glu Val Leu	Arg Lys Phe Arg Ala				
125		500		505		510		
126	cat gag acc	aac ctg ctt att	gca aca agt att	gta gaa gag ggt gtt		1584		
127	His Glu Thr	Asn Leu Leu Ile	Ala Thr Ser Ile	Val Glu Glu Gly Val				
128		515		520		525		
129	gat ata cca	aaa tgc aac ttg	gtg gtt cgt ttt	gat ttg ccc aca gaa		1632		
130	Asp Ile Pro	Lys Cys Asn Leu	Val Val Arg Phe	Asp Leu Pro Thr Glu				
131		530		535		540		
132	tat cga tcc	tat gtt caa tct	aaa gga aga gca	agg gca ccc atc tct		1680		
133	Tyr Arg Ser	Tyr Val Gln Ser	Lys Gly Arg Ala	Arg Ala Pro Ile Ser				
134	545		550		555		560	
135	aat tat ata	atg tta gcg gat	aca gac aaa ata	aaa agt ttt gaa gaa		1728		
136	Asn Tyr Ile	Met Leu Ala Asp	Thr Asp Lys Ile	Lys Ser Phe Glu Glu				
137		565		570		575		
138	gac ctt aaa	acc tac aaa gct	att gaa aag atc	ttg aga aac aag tgt		1776		
139	Asp Leu Lys	Thr Tyr Lys Ala	Ile Glu Lys Ile	Leu Arg Asn Lys Cys				
140		580		585		590		
141	tcc aag tcg	gtt gat act ggt	gag act gac att	gat cct gtc atg gat		1824		
142	Ser Lys Ser	Val Asp Thr Gly	Glu Thr Asp Ile	Asp Pro Val Met Asp				
143		595		600		605		
144	gat gat cac	gtt ttc cca cca	tat gtg ttg agg	cct gac gat ggt ggt		1872		
145	Asp Asp His	Val Phe Pro Pro	Tyr Val Leu Arg	Pro Asp Asp Gly Gly				
146		610		615		620		
147	cca cga gtc	aca atc aac acg	gcc att gga cac	atc aat aga tac tgt		1920		
148	Pro Arg Val	Thr Ile Asn Thr	Ala Ile Gly His	Ile Asn Arg Tyr Cys				
149	625		630		635		640	
150	gct aga tta	cca agt gat ccg	ttt act cat cta	gct cct aaa tgc aga		1968		
151	Ala Arg Leu	Pro Ser Asp Pro	Phe Thr His Leu	Ala Pro Lys Cys Arg				
152		645		650		655		

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154	Thr	Arg	Glu	Leu	Pro	Asp	Gly	Thr	Phe	Tyr	Ser	Thr	Leu	Tyr	Leu	Pro	
155				660					665					670			
156	att	aac	tca	cct	ctt	cga	gcc	tcc	att	ggt	ggt	cca	cca	atg	agc	tgt	2064
157	Ile	Asn	Ser	Pro	Leu	Arg	Ala	Ser	Ile	Val	Gly	Pro	Pro	Met	Ser	Cys	
158			675					680						685			
159	gta	cga	ttg	gct	gaa	aga	ggt	gtc	gct	ctc	att	tgc	tgt	gag	aaa	ctg	2112
160	Val	Arg	Leu	Ala	Glu	Arg	Val	Val	Ala	Leu	Ile	Cys	Cys	Glu	Lys	Leu	
161		690					695						700				
162	cac	aaa	att	ggc	gaa	ctg	gat	gac	cat	ttg	atg	cca	ggt	ggg	aaa	gag	2160
163	His	Lys	Ile	Gly	Glu	Leu	Asp	Asp	His	Leu	Met	Pro	Val	Gly	Lys	Glu	
164	705					710					715					720	
165	act	ggt	aaa	tat	gaa	gag	gag	ctt	gat	ttg	cat	gat	gaa	gaa	gag	acc	2208
166	Thr	Val	Lys	Tyr	Glu	Glu	Glu	Leu	Asp	Leu	His	Asp	Glu	Glu	Glu	Thr	
167				725						730					735		
168	agt	ggt	cca	gga	aga	cca	ggt	tcc	acg	aaa	cga	agg	cag	tgc	tac	cca	2256
169	Ser	Val	Pro	Gly	Arg	Pro	Gly	Ser	Thr	Lys	Arg	Arg	Gln	Cys	Tyr	Pro	
170			740						745					750			
171	aaa	gca	att	cca	gag	tgt	ttg	agg	gat	agt	tat	ccc	aga	cct	gat	cag	2304
172	Lys	Ala	Ile	Pro	Glu	Cys	Leu	Arg	Asp	Ser	Tyr	Pro	Arg	Pro	Asp	Gln	
173			755					760						765			
174	ccc	tgt	tac	ctg	tat	gtg	ata	gga	atg	ggt	tta	act	aca	cct	tta	cct	2352
175	Pro	Cys	Tyr	Leu	Tyr	Val	Ile	Gly	Met	Val	Leu	Thr	Thr	Pro	Leu	Pro	
176		770					775						780				
177	gat	gaa	ctc	aac	ttt	aga	agg	cgg	aag	ctc	tat	cct	cct	gaa	gat	acc	2400
178	Asp	Glu	Leu	Asn	Phe	Arg	Arg	Arg	Lys	Leu	Tyr	Pro	Pro	Glu	Asp	Thr	
179	785				790						795					800	
180	aca	aga	tgc	ttt	gga	ata	ctg	acg	gcc	aaa	ccc	ata	cct	cag	att	cca	2448
181	Thr	Arg	Cys	Phe	Gly	Ile	Leu	Thr	Ala	Lys	Pro	Ile	Pro	Gln	Ile	Pro	
182				805						810					815		
183	cac	ttt	cct	gtg	tac	aca	cgc	tct	gga	gag	ggt	acc	ata	tcc	att	gag	2496
184	His	Phe	Pro	Val	Tyr	Thr	Arg	Ser	Gly	Glu	Val	Thr	Ile	Ser	Ile	Glu	
185			820						825					830			
186	ttg	aag	aag	tct	ggt	ttc	atg	ttg	tct	cta	caa	atg	ctt	gag	ttg	att	2544
187	Leu	Lys	Lys	Ser	Gly	Phe	Met	Leu	Ser	Leu	Gln	Met	Leu	Glu	Leu	Ile	
188			835					840						845			
189	aca	aga	ctt	cac	cag	tat	ata	ttc	tca	cat	att	ctt	cgg	ctt	gaa	aaa	2592
190	Thr	Arg	Leu	His	Gln	Tyr	Ile	Phe	Ser	His	Ile	Leu	Arg	Leu	Glu	Lys	
191		850					855							860			
192	cct	gca	cta	gaa	ttt	aaa	cct	aca	gac	gct	gat	tca	gca	tac	tgt	ggt	2640
193	Pro	Ala	Leu	Glu	Phe	Lys	Pro	Thr	Asp	Ala	Asp	Ser	Ala	Tyr	Cys	Val	
194	865				870						875					880	
195	cta	cct	ctt	aat	ggt	ggt	aat	gac	tcc	agc	act	ttg	gat	att	gac	ttt	2688
196	Leu	Pro	Leu	Asn	Val	Val	Asn	Asp	Ser	Ser	Thr	Leu	Asp	Ile	Asp	Phe	
197			885							890					895		
198	aaa	ttc	atg	gaa	gat	att	gag	aag	tct	gaa	gct	cgc	ata	ggc	att	ccc	2736
199	Lys	Phe	Met	Glu	Asp	Ile	Glu	Lys	Ser	Glu	Ala	Arg	Ile	Gly	Ile	Pro	
200			900						905					910			
201	agt	aca	aag	tat	aca	aaa	gaa	aca	ccc	ttt	ggt	ttt	aaa	tta	gaa	gat	2784

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205 Tyr Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro
206      930          935          940
207 cat cga ttt tat gta gct gat gtg tac act gat ctt acc cca ctc agt      2880
208 His Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser
209 945          950          955          960
210 aaa ttt cct tcc cct gag tat gaa act ttt gca gaa tat tat aaa aca      2928
211 Lys Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr
212          965          970          975
213 aag tac aac ctt gac cta acc aat ctc aac cag cca ctg ctg gat gtg      2976
214 Lys Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val
215          980          985          990
216 gac cac aca tct tca aga ctt aat ctt ttg aca cct cga cat ttg aat      3024
217 Asp His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn
218      995          1000          1005
219 cag aag ggg aaa gcg ctt cct tta agc agt gct gag aag agg aaa      3069
220 Gln Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys
221      1010          1015          1020
222 gcc aaa tgg gaa agt ctg cag aat aaa cag ata ctg gtt cca gaa      3114
223 Ala Lys Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu
224      1025          1030          1035
225 ctc tgt gct ata cat cca att cca gca tca ctg tgg aga aaa gct      3159
226 Leu Cys Ala Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala
227      1040          1045          1050
228 gtt tgt ctc ccc agc ata ctt tat cgc ctt cac tgc ctt ttg act      3204
229 Val Cys Leu Pro Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr
230      1055          1060          1065
231 gca gag gag cta aga gcc cag act gcc agc gat gct ggc gtg gga      3249
232 Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser Asp Ala Gly Val Gly
233      1070          1075          1080
234 gtc aga tca ctt cct gcg gat ttt aga tac cct aac tta gac ttc      3294
235 Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro Asn Leu Asp Phe
236      1085          1090          1095
237 ggg tgg aaa aaa tct att gac agc aaa tct ttc atc tca att tct      3339
238 Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile Ser Ile Ser
239      1100          1105          1110
240 aac tcc tct tca gct gaa aat gat aat tac tgt aag cac agc aca      3384
241 Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His Ser Thr
242      1115          1120          1125
243 att gtc cct gaa aat gct gca cat caa ggt gct aat aga acc tcc      3429
244 Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr Ser
245      1130          1135          1140
246 tct cta gaa aat cat gac caa atg tct gtg aac tgc aga acg ttg      3474
247 Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu
248      1145          1150          1155
249 ctc agc gag tcc cct ggt aag ctc cac gtt gaa gtt tca gca gat      3519
250 Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp

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VERIFICATION SUMMARY

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